

RAW SEQUENCE LISTING

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Application Serial Number: 10/538,840
Source: PCT
Date Processed by STIC: 06-22-2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/538,840

TIME: 10:15:14

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06222005\J538840.raw

3 <110> APPLICANT: N. V. Nutricia
 4 Schmitt, Joachim
 5 Boehm, GOnther
 6 Stahl, Bernd
 7 Schauer, Roland
 8 Tiralongo, Evelin
 9 Schrader, Silke
 11 <120> TITLE OF INVENTION: Trans-Sialidases obtained fromTyrpanosoma congolense
 13 <130> FILE REFERENCE: NUT-047-WO
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/538,840
 C--> 15 <141> CURRENT FILING DATE: 2005-06-13
 15 <150> PRIOR APPLICATION NUMBER: DE 10258400.1
 16 <151> PRIOR FILING DATE: 2002-12-13
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1491
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Trypanosoma congolense
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1491)
 30 <223> OTHER INFORMATION:
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 35 1 5 10 15
 37 agg gag gtt ata att ccg aat ggt cgt gtg gat gcc cac tac tcc cgc 96
 38 Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg
 39 20 25 30
 41 gtc gtt gat ccc act gtt gtt gcg aag ggt aat aac att tat gtt ctc 144
 42 Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu
 43 35 40 45
 45 gtt ggg cgg tac aat gtc acg cgg ggc tac tgg cac aat agg aac aac 192
 46 Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn
 47 50 55 60
 49 aag gct ggc ata gcc gat tgg gag ccc ttc gtg tac aag ggc acg gtg 240
 50 Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val
 51 65 70 75 80
 53 aac gtg ggc acg aag ggc aat gcc act gat gtg tcg atc agc tgg gag 288
 54 Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu
 55 85 90 95
 57 agg act gca ctg aag tcg ctg tac aac ttc ccg gtt tcg gga agc cct 336

(Pg-6)

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58	Arg	Thr	Ala	Leu	Lys	Ser	Leu	Tyr	Asn	Phe	Pro	Val	Ser	Gly	Ser	Pro	
59				100					105					110			
61	ggc	acg	cag	ttc	ctt	gga	ggg	gct	ggg	ggt	ggt	gtt	gta	aca	tcc	aac	384
62	Gly	Thr	Gln	Phe	Leu	Gly	Gly	Ala	Gly	Gly	Gly	Val	Val	Thr	Ser	Asn	
63			115					120					125				
65	ggg	acg	att	gtg	ctg	cca	gtg	cag	gca	agg	aac	aag	gcc	aac	cgt	gtt	432
66	Gly	Thr	Ile	Val	Leu	Pro	Val	Gln	Ala	Arg	Asn	Lys	Ala	Asn	Arg	Val	
67		130					135				140						
69	gtg	agc	atg	atc	ctg	tac	tcg	gct	gac	gat	gga	aag	tca	tgg	cac	ttt	480
70	Val	Ser	Met	Ile	Leu	Tyr	Ser	Ala	Asp	Asp	Gly	Lys	Ser	Trp	His	Phe	
71	145					150				155					160		
73	ggg	aag	ggt	gag	gcc	ggt	gta	ggc	acg	tcc	gag	gct	gcc	ctc	act	gag	528
74	Gly	Lys	Gly	Glu	Ala	Gly	Val	Gly	Thr	Ser	Glu	Ala	Ala	Leu	Thr	Glu	
75				165					170				175				
77	tgg	gac	ggc	aag	ctg	ctg	att	agt	gca	cga	tcc	gat	ggt	gga	cag	ggc	576
78	Trp	Asp	Gly	Lys	Leu	Leu	Ile	Ser	Ala	Arg	Ser	Asp	Gly	Gly	Gln	Gly	
79			180					185					190				
81	tac	cgc	atg	ata	ttc	gaa	tcg	agt	gac	ctt	ggt	gcg	acg	tgg	aaa	gag	624
82	Tyr	Arg	Met	Ile	Phe	Glu	Ser	Ser	Asp	Leu	Gly	Ala	Thr	Trp	Lys	Glu	
83		195					200				205						
85	atg	ctc	aac	agc	atc	tcc	cgc	gtg	att	ggc	aac	tct	ccg	ggt	cgc	agt	672
86	Met	Leu	Asn	Ser	Ile	Ser	Arg	Val	Ile	Gly	Asn	Ser	Pro	Gly	Arg	Ser	
87		210				215				220							
89	ggt	cct	ggc	agc	tcg	agt	ggc	ttc	atc	acg	gtg	aca	gtg	gag	ggt	gtg	720
90	Gly	Pro	Gly	Ser	Ser	Ser	Gly	Phe	Ile	Thr	Val	Thr	Val	Glu	Gly	Val	
91	225				230				235				240				
93	cct	gtg	atg	ctg	att	acc	cac	ccg	aag	aac	ctt	aag	ggc	tcg	tat	tat	768
94	Pro	Val	Met	Leu	Ile	Thr	His	Pro	Lys	Asn	Leu	Lys	Gly	Ser	Tyr	Tyr	
95			245					250				255					
97	cgg	gac	cgt	ctg	cag	ctg	tgg	atg	acg	gac	ggc	aat	cgt	atg	tgg	cat	816
98	Arg	Asp	Arg	Leu	Gln	Leu	Trp	Met	Thr	Asp	Gly	Asn	Arg	Met	Trp	His	
99			260					265				270					
101	gtc	ggg	cag	gtc	tct	gag	ggc	gac	gat	aac	agc	gct	tac	agc	tcc	ctg	864
102	Val	Gly	Gln	Val	Ser	Glu	Gly	Asp	Asp	Asn	Ser	Ala	Tyr	Ser	Ser	Leu	
103			275				280					285					
105	ctg	tac	act	ccg	gac	ggg	gtc	ctg	tac	tgc	ttg	cat	gag	cag	aac	att	912
106	Leu	Tyr	Thr	Pro	Asp	Gly	Val	Leu	Tyr	Cys	Leu	His	Glu	Gln	Asn	Ile	
107		290				295				300							
109	gat	gag	gtg	tac	agc	ctc	cac	ctt	gtg	cgc	ctt	gtg	gac	gag	ctg	aaa	960
110	Asp	Glu	Val	Tyr	Ser	Leu	His	Leu	Val	Arg	Leu	Val	Asp	Glu	Leu	Lys	
111	305				310				315			320					
113	agc	att	aaa	tca	acg	gct	ctg	gtg	tgg	aag	gca	cag	gac	gag	ctt	ctc	1008
114	Ser	Ile	Lys	Ser	Thr	Ala	Leu	Val	Trp	Lys	Ala	Gln	Asp	Glu	Leu	Leu	
115			325					330				335					
117	ctg	ggc	aac	tgc	ctc	ccg	ggc	gat	aaa	tac	gat	ccc	ggg	tgt	gac	ggc	1056
118	Leu	Gly	Asn	Cys	Leu	Pro	Gly	Asp	Lys	Tyr	Asp	Pro	Gly	Cys	Asp	Gly	
119			340					345				350					
121	atc	ccc	acc	gct	ggg	ctt	gcc	ggg	ctg	ctg	gta	gga	ccc	ctg	acg	gag	1104
122	Ile	Pro	Thr	Ala	Gly	Leu	Ala	Gly	Leu	Leu	Val	Gly	Pro	Leu	Thr	Glu	

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123          355          360          365
125 aag acg tgg ccc gac gcg tat cgg tgc gtg aac gct gca acc agc ggc      1152
126 Lys Thr Trp Pro Asp Ala Tyr Arg Cys Val Asn Ala Ala Thr Ser Gly
127          370          375          380
129 gct gtg agc act gct gaa ggc gtg cgg ctg gac gtg ggt ggc ggt ggc      1200
130 Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly Gly
131 385          390          395          400
133 cat gtt gtg tgg ccc gtg agt gag cag ggg cag gac cag cgg tat tac      1248
134 His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr
135          405          410          415
137 ttt acc aac agc gag ttc acg ctc gcc gtc acg gtg cgg ttt gac gag      1296
138 Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu
139          420          425          430
141 atg cca cgg ggg gag ctc ccg ttg ctg ggg ttt gtg aac cgc aaa ggg      1344
142 Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly
143          435          440          445
145 aag gtg aag aag ata ctg aag gtg tcg ctg agc ggg gtg gag tgg ctc      1392
146 Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu
147          450          455          460
149 ctg gca tac ggg aat gag tac aac agc aca gcc gct gag ccg ctg gac      1440
150 Leu Ala Tyr Gly Asn Glu Tyr Asn Ser Thr Ala Ala Glu Pro Leu Asp
151 465          470          475          480
153 gtg aac gag agc cac cag gtg gtg cta gcg ctt cac gac ggg atc gtc      1488
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155          485          490          495
157 tcc      1491
158 Ser
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163 <211> LENGTH: 497
164 <212> TYPE: PRT
165 <213> ORGANISM: Trypanosoma congolense
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170 1          5          10          15
173 Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg
174          20          25          30
177 Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu
178          35          40          45
181 Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn
182          50          55          60
185 Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val
186 65          70          75          80
189 Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu
190          85          90          95
193 Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro
194          100          105          110
197 Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn
198          115          120          125
201 Gly Thr Ile Val Leu Pro Val Gln Ala Arg Asn Lys Ala Asn Arg Val

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205 Val Ser Met Ile Leu Tyr Ser Ala Asp Asp Gly Lys Ser Trp His Phe
206 145      150      155      160
209 Gly Lys Gly Glu Ala Gly Val Gly Thr Ser Glu Ala Ala Leu Thr Glu
210      165      170      175
213 Trp Asp Gly Lys Leu Leu Ile Ser Ala Arg Ser Asp Gly Gly Gln Gly
214      180      185      190
217 Tyr Arg Met Ile Phe Glu Ser Ser Asp Leu Gly Ala Thr Trp Lys Glu
218      195      200      205
221 Met Leu Asn Ser Ile Ser Arg Val Ile Gly Asn Ser Pro Gly Arg Ser
222      210      215      220
225 Gly Pro Gly Ser Ser Ser Gly Phe Ile Thr Val Thr Val Glu Gly Val
226 225      230      235      240
229 Pro Val Met Leu Ile Thr His Pro Lys Asn Leu Lys Gly Ser Tyr Tyr
230      245      250      255
233 Arg Asp Arg Leu Gln Leu Trp Met Thr Asp Gly Asn Arg Met Trp His
234      260      265      270
237 Val Gly Gln Val Ser Glu Gly Asp Asp Asn Ser Ala Tyr Ser Ser Leu
238      275      280      285
241 Leu Tyr Thr Pro Asp Gly Val Leu Tyr Cys Leu His Glu Gln Asn Ile
242      290      295      300
245 Asp Glu Val Tyr Ser Leu His Leu Val Arg Leu Val Asp Glu Leu Lys
246 305      310      315      320
249 Ser Ile Lys Ser Thr Ala Leu Val Trp Lys Ala Gln Asp Glu Leu Leu
250      325      330      335
253 Leu Gly Asn Cys Leu Pro Gly Asp Lys Tyr Asp Pro Gly Cys Asp Gly
254      340      345      350
257 Ile Pro Thr Ala Gly Leu Ala Gly Leu Leu Val Gly Pro Leu Thr Glu
258      355      360      365
261 Lys Thr Trp Pro Asp Ala Tyr Arg Cys Val Asn Ala Ala Thr Ser Gly
262      370      375      380
265 Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly Gly
266 385      390      395      400
269 His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr
270      405      410      415
273 Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu
274      420      425      430
277 Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly
278      435      440      445
281 Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu
282      450      455      460
285 Leu Ala Tyr Gly Asn Glu Tyr Asn Ser Thr Ala Ala Glu Pro Leu Asp
286 465      470      475      480
289 Val Asn Glu Ser His Gln Val Val Leu Ala Leu His Asp Gly Ile Val
290      485      490      495
293 Ser
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 831
299 <212> TYPE: DNA

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300 <213> ORGANISM: Trypanosoma congolense
302 <220> FEATURE:
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310 1          5          10          15
312 ttc gat aca cgt tat ctt cgc gct tcc gac agc agt ctc ata gac aca      96
313 Phe Asp Thr Arg Tyr Leu Arg Ala Ser Asp Ser Ser Leu Ile Asp Thr
314          20          25          30
316 gct atg aaa tac agt gcc gat cag ggg aag acg tgg aaa act gaa atc     144
317 Ala Met Lys Tyr Ser Ala Asp Gln Gly Lys Thr Trp Lys Thr Glu Ile
318          35          40          45
320 ata ata aaa aat gct aga cta act gat aac ttt tcc cgc gtc gtt gat     192
321 Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp
322          50          55          60
324 cca acg gtt gtt gtt aag ggt gat aac ttg ttt att ttt gtt ggg agg     240
325 Pro Thr Val Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg
326 65          70          75          80
328 tac aac acc tca tct gcc cca tgg gtc tgg cag gaa aac ggt aaa gac     288
329 Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp
330          85          90          95
332 tgg gat gta ctg ttg tac aag gcc aag gtg agg aag gaa tca gcg ggt     336
333 Trp Asp Val Leu Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly
334          100          105          110
336 ggg gta cca tca gtg agc ttt aca tgg gac gaa ccc cta tac ctg aag     384
337 Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys
338          115          120          125
340 cat ctg ctc acc tct gtc ggt aaa ata gac ggc agg tcc ctc ata caa     432
341 His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln
342          130          135          140
344 tac att ggt ggc gtt gga aat ggt att gta aca ccg aaa ggt act atc     480
345 Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile
346 145          150          155          160
348 gtg ttt cca gtt cag gtt tta aac acc aac aaa tcc gtc atg aac atg     528
349 Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met
350          165          170          175
352 ctt ctg tat tca agt aac gac gga aaa acc tgg gag ttc agc aaa act     576
353 Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr
354          180          185          190
356 tcc aca ccc gcg ggc aca act gag gcc tcc ctt gtt tgg tgg gat gga     624
357 Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly
358          195          200          205
360 caa cta ctt ctc aca agc aga aca act ccg gat gtc ggc agc cgc aaa     672
361 Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys
362          210          215          220
364 gta tat tta aca agc gac ctc gga act tca tgg aat gaa gcg atc gga     720

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30

L:307 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:305